

GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2003, 02:07:45 ; Search time 2645.71 seconds
 (without alignments) 1579.326 Million cell updates/sec

Title: US-09-698-781-3

Perfect score: 1436
 Sequence: 1MKQILHAPLETTAATLTFPVVL.....KHOVLVRDSCASKACNCNSIY 258

Scoring table: BLOSUM62

Xgapext 10.0 , Xgapext 0.5
 Ygapext 10.0 , Ygapext 0.5
 Fgapext 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Model_p2n.model -DEVLXH
 -Q=/cgn2.1/US9698781/runat_07032003_083459_5329/app_query.fasta_1.654
 -DB-EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -IOPEXT=0
 -UNITS-bits -START-1 -END-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR SCORE-PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTPMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US09698781-QC0N_1-12465-6runat_07032003_083459_5329 -NCPU=6 -ICPU=3
 -NO_XLXPY -NO_MMAP -LARGEQUERY -NEG SCORES -WAIT -LONGLOG -DEV TIMEOUT=120
 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: em_estba:*

2: em_estthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estio:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_p1n:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_main:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	965	67.2	547	9 AL703262	AL703262 DRK2P6986K
2	943	65.7	1037	13 BM55122	BM55122 AGENCOURT
3	943	65.7	1108	13 BM552843	BM552843 AGENCOURT
4	912	63.5	1063	13 BM557970	BM557970 AGENCOURT
5	869	60.5	803	13 603070694	BI859740 AGENCOURT
6	867	60.4	450	12 BF897404	BF897404 IL2-MT018
7	867	60.4	808	13 BI826967	BI826967 603077463
8	858	59.7	462	12 BF893777	BF893777 IL2-MT018
9	858	59.7	781	13 BI82771	BI82771 603079842
10	850	59.2	464	12 BF894110	BF894110 IL2-MT018
11	830	57.8	451	12 BF89412	BF89412 IL2-MT018
12	825	57.5	443	12 BF897401	BF897401 IL2-MT018
13	823.5	57.3	904	13 BI830749	BI830749 603075145
14	814	56.7	420	12 BF893778	BF893778 IL2-MT018
15	814	56.7	784	13 BI825564	BI825564 603072524
16	807.5	56.2	946	13 BI833557	BI833557 603072889
17	796	55.4	454	12 BF897368	BI897368 IL2-MT018
18	782.5	54.5	728	13 BI827352	BI827352 603077880
19	780	54.3	806	13 BI826010	BI826010 603076409
20	772.5	53.6	1414	11 AK00449	AK00449 Mus muscu
21	769	53.6	406	12 BF897379	BF897379 IL2-MT018
22	761	53.1	952	12 BG723420	BG723420 60269475
23	761.5	53.0	784	13 BI829333	BI829333 603079465
24	761.5	53.0	864	13 BI460544	BI460544 603201164
25	758	52.8	760	12 BG723432	BG723432 602693332
26	748	52.1	801	13 BI831850	BI831850 603078978
27	741	51.6	764	13 BI829788	BI829788 603079859
28	740	51.5	742	12 BG723701	BG723701 602697894
29	739	51.5	722	13 BI460734	BI460734 603204913
30	737	51.3	730	13 BI559392	BI559392 603253072
31	736	51.3	721	13 BI830127	BI830127 603072754
32	729	50.8	769	13 BI829992	BI829992 603076580
33	719.5	50.1	865	12 BG723720	BG723720 602698722
34	710.5	49.5	708	13 BI560558	BI560558 603254638
35	705	49.2	740	12 BG724382	BG724382 602692860
36	706.5	49.2	821	12 BG723866	BG723866 602695346
37	706	49.2	401	12 BF897366	BF897366 IL2-MT018
38	696	48.5	852	13 BI55321	BI55321 603106580
39	695.5	48.4	843	12 BG725588	BG725588 602694310
40	692.5	48.2	705	13 BI63698	BI63698 60306294
41	689.0	48.0	769	13 BI466694	BI466694 60320325
42	679.5	47.3	849	13 BI562149	BI562149 603253338
43	666.9	46.9	600	10 BE59808	BE59808 19697308
44	671.5	46.8	674	13 BI695604	BI695604 603307276
45	670	46.7	870	13 BI465248	BI465248 603204748

ALIGNMENTS

RESULT 1
 AL703262 LOCUS AL703262 547 bp mRNA linear EST 22-MAR-2002
 DEFINITION DKFP686K1819_r1 686 (synonym: h1cc3) Homo sapiens cDNA clone
 ACCESSION DKFP686K1819_5', mRNA sequence.
 VERSION AL703262.1
 KEYWORDS EST
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammal; Eutheria; Primates; Catarrhini; Homidae; Homo.
 (bases 1 to 547)
 AUTHORS Poustka,A., Wellenreuther,R., Meves,H.W., Weil,B. and Wiemann,S.
 TITLE EST (Poustka,A., Wellenreuther,R., Meves,H.W., Weil,B. and Wiemann,
 1998)

Qy	213	AspGlyLeuCysThrAspGlyCysLysTyrGluAspLeuTyrSerAspCysLysSerLeu	232	Qy	33	AlaAsnGluAspLysAspProAlaPheThrAlaLeuLeuThrThrGluThrGlnValGln	52
Db	730	AAGGACTATGGCCACCATAGTGGCAGATCAAGTCCTCAACTAAGTGATTCCTG	789	Db	229	GCA--GAAGGAAGGAAACGCCCTTACTGCCTGTTAACCCACCCAGTCAGTGAA	285
Qy	233	LysLeuThrLeuThrCysLysHisGlnLeuValArgAspSerCysLysAlaSerCysAla	252	Qy	53	ArgGluIleValAsnLysHisAsnGlnLeuValArgAlaValSerProAlaArgAsn	72
Db	790	AGATACAGCTGGC-TGTTAACATGAGTTACTCAAGGAAAGTGNCAAGCTACTTGCCA	848	Db	286	AGGAGATGTTAAATACACATGAACTTAAGGAAGGATCTCTCACCTGCGCAAGTAC	345
Qy	253	Cys 253	Db	849	TGT 851	Db	346
Qy	RESULT 4	BM559790	1063 bp	mRNA	linear	EST 20-FEB-2002	Qy
LOCUS	BM559790						93
DEFINITION	AGENCOURT 6565524 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5744414						Qy
ACCESSION	5', mRNA sequence.						Db
VERSION	BM559790						405
KEYWORDS	EST.						Db
SOURCE	human.						406
ORGANISM	Homo sapiens						TGCACTTACACATACAGTCAGTCAGGACGCCAACCGTACAAAGTGTGGAGAT
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						465
AUTHORS	(bases 1 to 1063)						Qy
TITLE	NIH_MGC http://mgc.nci.nih.gov/.						113
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)						LeuTyMetSerSerAlaProSerSerTrpSerGlnAlaLeuGlnSerTrpHeAspGlu
COMMENT	Unpublished (1999)						132
CONTACT	Contact: Robert Strausberg, Ph.D.						CTCTATATGTTAACTGACCGCTACTTCCTGCTCTGCAATCAACGCTGGTGTGACG
Email:	crapbs-r@mail.nih.gov						525
Tissue	Procurement: Life Technologies, Inc.						Qy
Procurement:	CDNA Library Preparation: Life Technologies, Inc.						133
CDNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)						ATCTAGATTTGTCTATGGCTAGGACAAAGTCCAAAGTGGGCCAACAG
DNA	Sequencing by: Agencourt Bioscience Corporation						905
Clone	Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:						CYSASNTYRAAGHISSerAsnProLysAspArgMetThrSerLeuLysCysGlyGluAsn
found	http://image.llnl.gov						112
through	Plate: LLM12165	row: 1	column: 15				Qy
the	High quality sequence stop: 618.						Db
I.	1. 1063						406
Location/Qualifiers	/organism="Homo sapiens"						TGCACTTACACATACAGTCAGTCAGGACCTTCTGCTCTGCAATATGTC
/db_xref="taxon:9606"							465
/clone="IMAGE:5744414"							Qy
/clone_1db="NIH_MGC_119"							153
/feature_type="mendelian"							ThrGluValValTrpTyrSerSerTy-LeuValGlyCysGlyAsnAlaTyrcyProAsn
/lab_host="DHIB"							172
/lab="DHIB"							Db
Qy	586	ACTCAGCTGTGTGACTCGACTTCCAGGTAGCTGCTGIGGATCTACTGTC	645	Qy	173	GlnLysValleuLysTrtyTrtyTrvalCysGlnTrcycyProAlaGlyAsnTrpAlaAsn	192
Db	706	AGAAAGATAACCCGACCCACAGACACCTTGTCGGGTCCTGATGACTTGAC	765	Db	646	CAAGATAGTGTCTAACTACTATGTTGCCAAATATGTCCTGCTGTTAAATATGAT	705
Qy	766	AAGGACTATGGCCACCATAGTGCAGATCAGATCTCTAAAGACTGGAAATRCCTT	825	Db	766	Qy	213
Db	826	GAAGATACAGCTGGGAAACCATGAGTACTCAAGGAAAG-TGGAGGCTACTTG	882	Db	826	AspGlyLeuCysThrAsnGlyCysLysTyrGluAspLeuTyrSerAsnCysLys-SerLeu	232
Qy	232	ulysleuThrLeuThrCysLysHisGlnLeuValArgAspSerCysAlaSerCys	251	Qy	193	ArgLeuTyrvAlProTyrglLgylAlaProCysAlaSerCysProAspAsnCysYasp	212
Db	8182346						Db
Qy	8182346						193
LOCUS	BI826345						ArgLeuTyrvAlProTyrglLgylAlaProCysAlaSerCysProAspAsnCysYasp
DEFINITION	DEFINITION						212
0070604F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5168015	0070604F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5168015						Db
mRNA sequence.	mRNA sequence.						766
B1826346	B1826346						Qy
VERSION	B1826346.1						232
KEYWORDS	EST.						Db
SOURCE	human.						826
ORGANISM	Homo sapiens						GAAGATACAGCTGGGAAACCATGAGTACTCAAGGAAAG-TGGAGGCTACTTG
Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						882
REFERENCE	Unpublished (1999)						Qy
COMMENT	Contact: Robert Strausberg, Ph.D.						113
Email:	crapbs-r@mail.nih.gov						LeuTyMetSerSerAlaProSerSerTrpSerGlnAlaLeuGlnSerTrpHeAspGlu
Tissue	Tissue Procurement: Life Technologies, Inc.						132
Procurement:	CDNA Library Preparation: Life Technologies, Inc.						CTCTATATGTTAACTGACCGCTACTTCCTGCTCTGCAATATGTC
CDNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)						525
DNA	Sequencing by: Incyte Genomics, Inc.						Qy
Clone	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:						153
found	http://image.llnl.gov						ThrGluValValTrpTyrSerSerTy-LeuValGlyCysGlyAsnAlaTyrcyProAsn
through	Plate: LLM1417	row: k	column: 24				172
the	High quality sequence stop: 799.						ACTCAGCTGTGTGACTCGACTTCCAGGTAGCTGCTGIGGATCTACTGTC

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br		
FEATURES	High quality sequence stop: 450. Location/Qualifiers		
SOURCE	1. 451 'organism' "Homo sapiens" 'db_xref' "taxon:9606" 'clone_1lib' "MT0181" 'dev_stage' "Adult" 'note' "Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
BASE COUNT	130 a 94 c 92 g 131 t 4 others		
ORIGIN			
Alignment Scores:			
Pred. No.:	8.69e-84	Length:	451
Score:	830.00	Matches:	144
Percent Similarity:	97.97%	Conservative:	1
Best Local Similarity:	97.30%	Mismatches:	3
Query Match:	57.80%	Indels:	0
DB:	12	Gaps:	0
US-09-698-781-3 (1-258) x BF897412 (1-451)			
QY	111 GluAsnLeuTyRMetSerSerAlaProSerSerTrpSerGlnAlaLeuGlnSerTrpHe	Length:	130
Db	'		
Db	31 TCGAAATTGTTCAACAGSCATTAT 8		
RESULT	12		
REF ID	BF897401/C		
LOCUS	BF897401 443 bp mRNA linear EST 18-JAN-2001		
DEFINITION	IL2-MT0181-281100-265-D11 MT0181 Homo sapiens CDNA, mRNA sequence.		
ACCESSION	BF897401		
VERSION	BF897401.1 GI-12288847		
KEYWORDS	EST.		
ORGANISM	Human.		
JOURNAL	Molecular Biology and Evolution 18: 18-23 (2001)		
MEDLINE	12024663		
REFERENCE	1 (bases 1 to 443)		
AUTHORS	Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordim, S., Costa, F.F., Goldman, G.H., Cavalho, A.F., Matsukuma, A., Bafia, G.S., Simpson, D.H., Brunstein, A., Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, S.J. and Simpson, A.J.		
COMMENT	Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br		
FEATURES	High quality sequence stop: 406.		
SOURCE	1. 443 'organism' "Homo sapiens" 'db_xref' "taxon:9606" 'clone_1lib' "MT0181" 'dev_stage' "Adult" 'note' "Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
BASE COUNT	128 a 92 c 91 g 130 t 2 others		
ORIGIN			
Alignment Scores:			
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Score:	825.00	Matches:	142
Percent Similarity:	98.62%	Conservative:	1
Best Local Similarity:	97.93%	Mismatches:	2
Query Match:	57.45%	Indels:	0
DB:	12	Gaps:	0
US-09-698-781-3 (1-258) x BF897401 (1-443)			
QY	114 TyrMetSerSerAlaProSerSerTrpSerGlnAlaLeuGlnSerTrpHeAspGlyTyr 133		
Db	442 TACATGTCAGTGCNNCAAGCTCATGGTCAACAGCTTCAGGAACTCCACAGCTGTTGAGTAC 383		
QY	134 AsnAspPheAspGlyValGlyProLysSerAspSerGlyAspGlyValGlyHisTyrThr 153		
Db	382 AATGATTGTTGACTTGGTAGGSCCAAGACTCCCACTCAGTGTGTTGAGCATATTACA 323		
QY	251 CysAsnCysSerAsnSerIleTyr 258		

Qy 154 GlinalValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGln 173
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 Db 322 CAGGTTGTTGGTACTCTCATACCGTGGATGGAAATGCCACTCAA 263

Qy 174 LysValLeuTyrTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTyrAlaAsnArg 193
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 Db 262 AAAGTCTAAATACACTATGTTGCCATTATGCTGCTGTTAATGGCTATAGA 203

Qy 194 LeuTrpValPheTyrGluGlyGlyAlaProCysAlaSerCysProAspCysAspASP 213
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 Db 202 CTTATGTCCTTATGACAAGGAGACCTTGCCAGTGTGACAT 143

Qy 214 GlyLeuCysteProAsnGlyCysTyrGluAspLeuTyrSerAsnCysLysSerLys 233
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 Db 142 GCACTATGCAACCAATGCTGAGAGTCTCTATAGTAAAGTTGAAG 83

Qy 234 LeuThrLeuTyrCysLysGlnLeuValArgAspSerCysLysAlaSerCysAsnCys 253
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 Db 82 CTACATTAACCTGTAAACATCAGTGTGTCAGGAGACGTGCAAGTGT 23

Qy 254 SerAsnSerIleTyr 258
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 Db 22 TCAAACAGCATTTAT 8

RESULT 13

B1830749 DEFINITION 6030751451 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5167186 5', mRNA sequence.

ACCESSION B1830749
 VERSION EST.
 KEYWORDS human.
 SOURCE
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 904)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgsabst@nlm.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://Image.llnl.gov
 Plate: ILM1415 row: 1 column: 11
 High quality sequence stop: 827.

FEATURES source
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 /db_xref="taxon:9606"
 /clone="IMAGE:5167186"
 /clone_11b="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organism: brain; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source: normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
 BASE COUNT 278 a 201 c 193 g 232 t
 ORIGIN Alignment Scores: 1.47e-82 Length: 904
 Pred. No.:

Score: 823.50
 Percent Similarity: 75.95%
 Best Local Similarity: 64.89%
 Query Match: 13
 DB: 13
 Gaps: 5

US-09-698-781-3 (1-258) x B1830749 (1-904)

Qy 1 MetLysGlnIleLeuHisProLeuLeuGluThr-Thr----AlaMetThrLeuPhePr 18
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 Db 125 ATAAAGTAGATATTTCATCCCTCTGCAAGAACACATTTCAGCAGTGGTTACTAC 184

Qy 18 ovalLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLys 38
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 Db 239 TCCGCCTTACTGCTGTTAACACCCAGTCAGTGCAGTGCAGGAGTTGAAATAA 298

Qy 58 SHISASGluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluT 78
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 Db 299 AGCAATGACTAAGGAGAGTCCTCCACTGCGCATCTGATGATGGATG 358

Qy 78 pasnLysGluAlaAlaAsnAlaGlnLysTpaAsnGlnCysAsnTyrArgISe 98
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 359 GAGCAGAGAGGTACACAGAATGCCAAAGGGGGCAACAGTGTCACTTACAACATAG 418

Qy 98 rAsnProLysAspArgMetThrSerIleLysCysGlyGluAsnLeuTrpMetSerSerAl 118
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 Db 419 TGATCCAGGAGCCAAACCGTCAAGATGCTGGAGAATCTATGTCAGTA 478

Qy 118 aproSerSerTyrSerCysGlnAlaIleGlnSerTyrPheAspGluTyrAsnAspPheAspPh 138
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 Db 479 CCCTACTCTCCTGCTCTGCAATCCAAAGCTGGTAAAG 537

Qy 138 eGlyLysGlyProLysThrProAsnAlaValValGlyHisTyrGlyValValTrpT 158
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 Db 598 CTGCACTTACCGTGGATGCTGGAATGCCCAATCAGATGCTAAATA 657

Qy 178 TrpTyrValCysGlnTyrCysProAlaGlyAsnTyrAlaAsnArgLeuTyrValProT 198
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 Db 658 CTACTATGTTTCCCATATGTCGCTGCTGTTAATATGATAAGATAACCGT 717

Qy 198 YrgLugLysGlyAlaProCysAlaSerCysProAspCysAspAspGly--LeuCys 216
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 Db 718 ACCAACAGGAACACCTGTGGCGGTGCGCTGTGACTAAAGGACTATGTGCG 777

Qy 217 ThrasnGlyCysLysTyrGluAsp--LeuTrpSerAsnCysLysLeuLysLeuThrL 236
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 Db 778 ACCAATGTTGCCAGTATCAGAAATCTCTTAAAGTGTGATCTTGCAGAAATT 837

Qy 236 euthrCys----LysHisGlnLeuValArgAspSerCysLysAlaSerCys 251
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 Db 838 ACAGCTGGTGTGACACATGAGTACTCAGCGAAAGTGGCAGGTACTTGC 991

RESULT 14

BF897378 DEFINITION IL2-MT0181-281100-265-A06 MT0181 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF897378
 VERSION BF897378.1 GI:1228837
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 420)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,

QY	207	CysProAspAsnCysAspAspGlyLeuCysThrAspGlyCysLysTyrGlusIeu	225
Db	362	I I I I I I I I I I	418
COMMENT		TITLE	Shotgun sequencing of the human transcriptome with ORF expressed
MEDLINE		JOURNAL	sequence tags
		PROC.	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
		CONTACT	Simpson, A.J.G.
		LABORATORY	Ludwig Institute for Cancer Genetics
		RUA PROF.	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
		TEL:	+55-11-2704922
		FAX:	+55-11-2707001
		EMAIL:	asimpson@ludwig.org.br
		THIS SEQUENCE WAS DERIVED FROM THE FAPESP/LICR HUMAN CANCER GENOME PROJECT. THIS ENTRY CAN BE SEEN IN THE FOLLOWING URL (HTTP://WWW.LUDWIG.ORG.BR/SCRIPTS/GETHTML2.PL?TI=IL2&T2=IL2-MT0181-281100-655-A00873=2000-11-28&TI=1)	
		SEQ PRIMER:	puc 18 forward
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		/note="Organ: marrow; Vector: puc18; Site_1: Smal; Site_2: SmaI; A mini-library was made by cloning products derived from ORESSES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	
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QY	87	GlyLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArgMetThrSer	106
Db	2	I I I I I I I I I I	61
QY	107	LeuLysCysGlnGluAsnLeuTyrMetSerSerAlaProSerSerTnPSerGlnAlaLe	126
Db	62	CTAAATGTCGCGAGAATCTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC	121
QY	127	GlnSerTrpPheAspGluTyrAsnAspHeAspHeAspHeGlyValGlyProLysAlaPro	146
Db	122	I I I I I I I I I I	181
QY	147	AlaAlaValValGlyLysTyrThrGlnValAlaValTyrTyrSerSerTyrLeuValAlaLe	166
Db	182	I I I I I I I I I I	241
QY	167	AsnAlaTyrCysProAspGlnGlyValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	186
Db	242	ATGGCTTACTGTCGCCAACTCAAAAGTCTAAATACTACTACTGTTGTCCTAAATGTC	301
QY	187	AlaGlyAspTrpAlaAsnArgLeuTyrAlaProTyrGluGlyValAlaProCysAlaSer	206
Db	302	GCTGGTAATGGCTAATGACCTATGTCCTATGACAAAGGACCTGTCAGTGC	361
QY	207	CysProAspAsnCysAspAspGlyLeuCysThrAspGlyCysLysTyrGlusIeu	225
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		SEQ PRIMER:	puc 18 forward
		HIGH QUALITY SEQUENCE STOP:	397.
FEATURES	source	LOCATION/QUALIFIERS	
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		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/clone_id="MT0181"	
		/dev_stage="Adult"	
		/note="Organ: marrow; Vector: puc18; Site_1: Smal; Site_2: SmaI; A mini-library was made by cloning products derived from ORESSES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	
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		ALIGNMENT SCORES:	
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		PERCENT SIMILARITY:	100.00%
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BASE COUNT	US-09-698-781-3 (1-258) x B1897378 (1-420)	ORIGIN	
QY	87	GlyLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArgMetThrSer	106
Db	2	I I I I I I I I I	61
QY	107	LeuLysCysGlnGluAsnLeuTyrMetSerSerAlaProSerSerTnPSerGlnAlaLe	126
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QY	187	AlaGlyAspTrpAlaAsnArgLeuTyrAlaProTyrGluGlyValAlaProCysAlaSer	206
Db	302	GCTGGTAATGGCTAATGACCTATGTCCTATGACAAAGGACCTGTCAGTGC	361
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		SEQ PRIMER:	puc 18 forward
		HIGH QUALITY SEQUENCE STOP:	397.
FEATURES	source	LOCATION/QUALIFIERS	
	1.	420	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
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BASE COUNT	127	a	90 c 91 g 112 t
ORIGIN			
		ALIGNMENT SCORES:	
		PRED. NO.:	5.03e-82
		SCORE:	84.00
		PERCENT SIMILARITY:	100.00%
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		QUERY MATCH:	56.69%
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BASE COUNT	US-09-698-781-3 (1-258) x B1897378 (1-420)	ORIGIN	
QY	87	GlyLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArgMetThrSer	106
Db	2	I I I I I I I I I	61
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Db	122	I I I I I I I I I	181
QY	147	AlaAlaValValGlyLysTyrThrGlnValAlaValTyrTyrSerSerTyrLeuValAlaLe	166
Db	182	I I I I I I I I I	241
QY	167	AsnAlaTyrCysProAspGlnGlyValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	186
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QY	187	AlaGlyAspTrpAlaAsnArgLeuTyrAlaProTyrGluGlyValAlaProCysAlaSer	206
Db	302	GCTGGTAATGGCTAATGACCTATGTCCTATGACAAAGGACCTGTCAGTGC	361
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FEATURES	source	LOCATION/QUALIFIERS	
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BASE COUNT	127	a	174 c 165 g 201 t
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Db	137	I I I I I I I I I I	195
QY	18	ProValLeuLeuIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	37
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